

10/550671

1/13 **JC20 Rec'd PCT/PTO 26 SEP 2009**

SEQUENCE LISTING

<110> Arkray, Inc.

<120> Method for producing glucose dehydrogenase

<130> G843-OPC4051

<150> JP 2003-82739

<151> 2003-03-25

<160> 15

<170> PatentIn Ver. 2.0

<210> 1

<211> 2467

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (258)..(761)

<220>

<221> CDS

<222> (764)..(2380)

<220>

<221> CDS

<222> (2386)..(2466)

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tacgaatggc tgacacatgt aatggactat aaaaccatgt tccgttccgg aatgtgcgcg 180

tacatttcag gtccgcgcgc attttgaga aatatcaagc gtggtttcc cgaatccgg 240

gttcgagaga aggaaac aig cac aac gac act ccc cac tcg cgt cgc 290

Met His Asn Asp Asn Thr Pro His Ser Arg Arg

1

5

10

cac ggc gac gca gcc gca tca ggc atc acg cgg cgt caa tgg ttg caa 338

His Gly Asp Ala Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln

15

20

25

ggc gcg ctg gcg ctg acc gca gcg ggc ctc acg ggt tcg ctg aca ttg		386	
Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu			
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cgg gcg ctt gca gac aac ccc ggc act gcg ccg ctc gat acg ttc atg		434	
Arg Ala Leu Ala Asp Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met			
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acg ctt tcc gaa tcg ctg acc ggc aag aaa ggg ctc agc cgc gtg atc		482	
Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile			
60	65	70	75
ggc gag cgc ctg ctg cag gcg ctg cag aag ggc tcg ttc aag acg gcc		530	
Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala			
80	85	90	
gac agc ctg ccg cag ctc gcc ggc ctc gcg tcc ggt tcg ctg acg		578	
Asp Ser Leu Pro Gln Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr			
95	100	105	
cct gaa cag gaa tcg ctc gca ctg acg atc ctc gag gcc tgg tat ctc		626	
Pro Glu Gln Glu Ser Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu			
110	115	120	
ggc atc gtc gac aac gtc gtg att acg tac gag gaa gca tta atg ttc		674	
Gly Ile Val Asp Asn Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe			
125	130	135	
ggc gtc gtg tcc gat acg ctc gtg atc cgt tcg tat tgc ccc aac aaa		722	
Gly Val Val Ser Asp Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys			
140	145	150	155
ccc ggc ttc tgg gcc gac aaa ccg atc gag agg caa gcc tg atg gcc		769	
Pro Gly Phe Trp Ala Asp Lys Pro Ile Glu Arg Gln Ala Met Ala			
160	165	170	
gat acc gat acg caa aag gcc gac gtc gtc gtt gga tcg ggt gtc		817	
Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser Gly Val			
175	180	185	
gcg ggc gcg atc gtc gcg cat cag ctc gcg atg gcg ggc aag gcg gtg		865	
Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys Ala Val			
190	195	200	
atc ctg ctc gaa gcg ggc ccg cgc atg ccg cgc tgg gaa atc gtc gag		913	
Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile Val Glu			
205	210	215	
cgc ttc cgc aat cag ccc gac aag atg gac ttc atg gcg ccg tac ccg		961	
Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro Tyr Pro			
220	225	230	
tcg agc ccc tgg gcg ccg cat ccc gag tac ggc ccg ccg aac gac tac		1009	
Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn Asp Tyr			
235	240	245	250
ctg atc ctg aag ggc gag cac aag ttc aac tcg cag tac atc cgc gcg		1057	

Leu	Ile	Leu	Lys	Gly	Glu	His	Lys	Phe	Asn	Ser	Gln	Tyr	Ile	Arg	Ala	
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gtg	ggc	ggc	acg	acg	tgg	cac	tgg	gcc	gcg	tcg	gcg	tgg	cgc	ttc	att	1105
Val	Gly	Gly	Thr	Thr	Trp	His	Trp	Ala	Ala	Ser	Ala	Trp	Arg	Phe	Ile	
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ccg	aac	gac	ttc	aag	atg	aag	agc	gtg	tac	ggc	gtc	ggc	cgc	gac	tgg	1153
Pro	Asn	Asp	Phe	Lys	Met	Lys	Ser	Val	Tyr	Gly	Val	Gly	Arg	Asp	Trp	
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ccg	atc	cag	tac	gac	gat	ctc	gag	ccg	tac	tat	cag	cgc	gcg	gag	gaa	1201
Pro	Ile	Gln	Tyr	Asp	Asp	Leu	Glu	Pro	Tyr	Tyr	Gln	Arg	Ala	Glu	Glu	
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gag	ctc	ggc	gtg	tgg	ggc	ccg	ggc	ccc	gag	gaa	gat	ctg	tac	tcg	ccg	1249
Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr	Ser	Pro	
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ccg	aag	cag	ccg	tat	ccg	atg	ccg	ccg	ctg	ccg	ttg	tcg	ttc	aac	gag	1297
Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe	Asn	Glu	
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cag	acc	atc	aag	acg	gcf	ctg	aac	aac	tac	gat	ccg	aag	ttc	cat	gtc	1345
Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe	His	Val	
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gtg	acc	gag	ccg	gtc	gcf	cgf	aac	agc	cgf	ccg	tac	gac	ggc	cgf	ccg	1393
Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly	Arg	Pro	
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act	tgt	tgc	ggc	aac	aac	aac	tgc	atg	ccg	atc	tgc	ccg	atc	ggc	gcf	1441
Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile	Gly	Ala	
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atg	tac	aac	ggc	atc	gtg	cac	gtc	gag	aag	gcc	gaa	cgf	gcc	ggc	gcf	1489
Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala	Gly	Ala	
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aag	ctg	atc	gag	aac	gcf	gtc	gtc	tac	aag	ctc	gag	acg	ggc	ccg	gac	1537
Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly	Pro	Asp	
																415
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aag	cgf	atc	gtc	gcf	gcf	ctc	tac	aag	gac	aag	acg	ggc	gcc	gag	cat	1585
Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala	Glu	His	
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cgf	gtc	gaa	ggc	aag	tat	ttc	gtg	ctc	gcc	gcf	aac	ggc	atc	gag	acg	1633
Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile	Glu	Thr	
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ccg	aag	atc	ctg	ctg	atg	tcc	gcf	aac	cgf	gat	ttc	ccg	aac	ggt	gtc	1681
Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn	Gly	Val	
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gcf	aac	agc	tcg	gac	atg	gtc	ggc	cgf	aac	ctg	atg	gac	cat	ccg	ggc	1729
Ala	Asn	Ser	Ser	Asp	Met	Val	Gly	Arg	Asn	Leu	Met	Asp	His	Pro	Gly	

475	480	485	490	
acc ggc gtg tcg ttc tat gcg agc gag aag ctg tgg ccg ggc cgc ggc				1777
Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly				
495	500	505		
ccg cag gag atg acg tcg ctg atc ggt ttc cgc gac ggt ccg ttc cgc				1825
Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro Phe Arg				
510	515	520		
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Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser Arg Ile				
525	530	535		
gac cag gag acg cag aag aag atc ttc aag gcc ggc aag ctg atg aag ccc				1921
Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met Lys Pro				
540	545	550		
gac gag ctc gac gct cag atc cgc gac cgt tcc gca cgc tac gtg cag				1969
Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr Val Gln				
555	560	565	570	
ttc gac tgc ttc cac gaa atc ctg ccg caa ccc gag aac cgc atc gtg				2017
Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val				
575	580	585		
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Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro Glu Ile				
590	595	600		
acg tat gct atc gac gac tac gtg aag cgc ggc gcc gct cat acg cgc				2113
Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg				
605	610	615		
gag gtc tac gct acc gcc gct aag gtg ctc ggc ggc acg gac gtc gtg				2161
Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp Val Val				
620	625	630		
ttc aac gac gaa ttc gct ccg aac aat cac atc acg ggc tcg acg atc				2209
Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser Thr Ile				
635	640	645	650	
atg ggc gcc gat gct cgc gac tcc gtc gtc gac aag gac tgc cgc acg				2257
Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys Arg Thr				
655	660	665		
ttc gac cat ccg aac ctg ttc att tcg acg acg gct acg atg ccg acc				2305
Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ala Thr Met Pro Thr				
670	675	680		
gtc ggt acc gta aac gtg acg ctg acg atc gcc gct ctc gct ctg cgg				2353
Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg				
685	690	695		
atg tcg gac acg ctg aag aag gaa gtc tgacc gtg cggt aaa tct act ctc				2403
Met Ser Asp Thr Leu Lys Lys Glu Val Val Arg Lys Ser Thr Leu				
700	705	710		

act ttc ctc atc gcc ggc tgc ctc gcg ttg ccg ggc ttc gcg cgc gcg	2451
Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe Ala Arg Ala	
715 720 725	
gcc gat gcg gcc gat c	2467
Ala Asp Ala Ala Asp	
730	

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 <212> PRT
 <213> Burkholderia cepacia

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 Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu Arg Ala Leu Ala Asp
 35 40 45
 Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser
 50 55 60
 Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu
 65 70 75 80
 Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln
 85 90 95
 Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser
 100 105 110
 Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn
 115 120 125
 Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp
 130 135 140
 Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys Pro Gly Phe Trp Ala
 145 150 155 160
 Asp Lys Pro Ile Glu Arg Gln Ala
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<210> 3
 <211> 539
 <212> PRT
 <213> Burkholderia cepacia

<400> 3
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Gly Val Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys
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Ala Val Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile
 35 40 45

Val Glu Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro
 50 55 60

Tyr Pro Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn
 65 70 75 80

Asp Tyr Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile
 85 90 95

Arg Ala Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg
 100 105 110

Phe Ile Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg
 115 120 125

Asp Trp Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala
 130 135 140

Glu Glu Glu Leu Gly Val Trp Gly Pro Gly Pro Glu Glu Asp Leu Tyr
 145 150 155 160

Ser Pro Arg Lys Gln Pro Tyr Pro Met Pro Pro Leu Pro Leu Ser Phe
 165 170 175

Asn Glu Gln Thr Ile Lys Thr Ala Leu Asn Asn Tyr Asp Pro Lys Phe
 180 185 190

His Val Val Thr Glu Pro Val Ala Arg Asn Ser Arg Pro Tyr Asp Gly
 195 200 205

Arg Pro Thr Cys Cys Gly Asn Asn Asn Cys Met Pro Ile Cys Pro Ile
 210 215 220

Gly Ala Met Tyr Asn Gly Ile Val His Val Glu Lys Ala Glu Arg Ala
 225 230 235 240

Gly Ala Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly
 245 250 255

Pro Asp Lys Arg Ile Val Ala Ala Leu Tyr Lys Asp Lys Thr Gly Ala
 260 265 270

Glu His Arg Val Glu Gly Lys Tyr Phe Val Leu Ala Ala Asn Gly Ile
 275 280 285

Glu Thr Pro Lys Ile Leu Leu Met Ser Ala Asn Arg Asp Phe Pro Asn
 290 295 300

Gly Val Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His
 305 310 315 320

Pro Gly Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly
 325 330 335

Arg Gly Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro
 340 345 350

Phe Arg Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser

355	360	365
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370	375	380
Lys Pro Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr		
385	390	395
Val Gln Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg		
405	410	415
Ile Val Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro		
420	425	430
Glu Ile Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His		
435	440	445
Thr Arg Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp		
450	455	460
Val Val Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser		
465	470	475
Thr Ile Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys		
485	490	495
Arg Thr Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met		
500	505	510
Pro Thr Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala		
515	520	525
Leu Arg Met Ser Asp Thr Leu Lys Lys Glu Val		
530	535	

<210> 4

<211> 27

<212> PRT

<213> Burkholderia cepacia

<400> 4

Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu			
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Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp			
20	25		

<210> 5

<211> 16

<212> PRT

<213> Burkholderia cepacia

<400> 5

Ala Asp Ala Ala Asp Pro Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala			
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<210> 6
<211> 25
<212> PRT
<213> Artificial Sequence.

<220>
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<220>
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<222> (6, 17, 18, 19, 22)
<223> Xaa=unknown

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 1 5 10 15
 Xaa Xaa Xaa Asp Cys Xaa Ala Cys His
 20 25

<210> 7
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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tgcaccgtgc ggaaatctac tctcact

27

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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27

<210> 9

<211> 1441

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (121)..(1398)

<400> 9

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gtg	cgg	aaa	tct	act	ctc	act	ttc	ctc	atc	gcc	ggc	tgc	ctc	gct	ttg	168
Val	Arg	Lys	Ser	Thr	Leu	Thr	Phe	Leu	Ile	Ala	Gly	Cys	Leu	Ala	Leu	
1	5		10		15											
ccg	ggc	ttc	gct	cgc	gct	gcc	gat	gct	ccg	gct	ctg	gtc	aag		216	
Pro	Gly	Phe	Ala	Arg	Ala	Ala	Asp	Ala	Asp	Ala	Asp	Pro	Ala	Leu	Val	Lys
20		25			30											
cgc	ggc	gaa	tac	ctc	gct	acc	gcc	atg	ccg	gtt	ccg	atg	ctc	ggc	aag	264
Arg	Gly	Glu	Tyr	Leu	Ala	Thr	Ala	Met	Pro	Val	Pro	Met	Leu	Gly	Lys	
35		40			45											
atc	tac	acg	agc	aac	atc	acg	ccc	gat	ccc	gat	acg	ggc	gac	tgc	atg	312
Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Met	
50		55			60											
gcc	tgc	cac	acc	gtg	aag	ggc	ggc	aag	ccg	tac	gct	ggc	ggc	ctt	ggc	360
Ala	Cys	His	Thr	Val	Lys	Gly	Gly	Lys	Pro	Tyr	Ala	Gly	Gly	Leu	Gly	
65		70			75									80		
ggc	atc	ggc	aaa	tgg	acg	ttc	gag	gac	ttc	gag	ccg	gct	gtg	ccg	cac	408
Gly	Ile	Gly	Lys	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His	
85		90			95											
ggc	gtg	tcg	aag	ggc	gac	aac	ctg	tat	ccg	gct	atg	ccg	tac	gtg		456
Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	Pro	Tyr	Val	
100		105			110											
tcg	tac	gct	aag	atc	aag	gac	gac	gta	ccg	gct	ctg	tac	gcc	tac		504
Ser	Tyr	Ala	Lys	Ile	Lys	Asp	Asp	Asp	Val	Arg	Ala	Leu	Tyr	Ala	Tyr	
115		120			125											
ttc	atg	cac	ggc	gtc	gag	ccg	gtc	aag	cag	gct	ccg	ccg	aag	aac	gag	552
Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu	
130		135			140											
atc	cca	gct	ctg	cta	agc	atg	ccg	tgg	ccg	ctg	aag	atc	tgg	aac	tgg	600
Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	Trp	Asn	Trp	
145		150			155									160		
ctg	ttc	ctg	aag	gac	ggc	ccg	tac	cag	ccg	aag	ccg	tct	cag	agc	gcc	648
Leu	Phe	Leu	Lys	Asp	Gly	Pro	Tyr	Gln	Pro	Lys	Pro	Ser	Gln	Ser	Ala	

165	170	175	
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc			696
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser			
180	185	190	
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac			744
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp			
195	200	205	
gaa acc ggc ggc agc ttc ctc gcg ggg tcg gtg ctc gcc ggc tgg gac			792
Glu Thr Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp			
210	215	220	
ggc tac aac atc acg tcg gac ccg aat gcg ggg atc ggc agc tgg acg			840
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr			
225	230	235	240
cag cag cag ctc gtg cag tat ttg cgc acc ggc agc gtg ccg ggc gtc			888
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val			
245	250	255	
gcg cag gcg gcc ggg ccg atg gcc gag gcg gtc gag cac agc ttc tcg			936
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser			
260	265	270	
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Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr			
275	280	285	
gtg ccg gcc gtt gcc gac agc aac gcg aag cag ccg cgg tcg tcg tgg			1032
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp			
290	295	300	
ggc aag ccg gcc gag gac ggg ctg aag ctg cgc ggt gtc gcg ctc gcg			1080
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala			
305	310	315	320
tcg tcg ggc atc gat ccg gcg cgg ctg tat ctc ggc aac tgc gcg acg			1128
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr			
325	330	335	
tgc cac cag atg cag ggc aag ggc acg ccg gac ggc tat tac ccg tcg			1176
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser			
340	345	350	
ctg ttc cac aac tcc acc gtc ggc gcg tcg aat ccg tcg aac ctc gtg			1224
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val			
355	360	365	
cag gtg atc ctg aac ggc gtg cag cgc aag atc ggc agc gag gat atc			1272
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile			
370	375	380	
ggg atg ccc gct ttc cgc tac gat ctg aac gac gac gcg cag atc gcc gcg			1320
Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala			
385	390	395	400

ctg acg aac tac gtg acc gcg cag ttc ggc aat ccg gcg gcg aag gtg	1368
Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val	
405	410
415	
acg gag cag gac gtc gcg aag ctg cgc tga catagtcggg cgcgccgaca	1418
Thr Glu Gln Asp Val Ala Lys Leu Arg	
420	425
cggcgcaacc gataggacag gag	1441

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 <211> 425
 <212> PRT
 <213> Burkholderia cepacia

<400> 10				
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu				
1	5	10	15	
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys				
20	25	30		
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys				
35	40	45		
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met				
50	55	60		
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly				
65	70	75	80	
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His				
85	90	95		
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val				
100	105	110		
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr				
115	120	125		
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu				
130	135	140		
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp				
145	150	155	160	
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala				
165	170	175		
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser				
180	185	190		
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp				
195	200	205		
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp				
210	215	220		
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr				

12/13

225	230	235	240												
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Val
245		250		255											
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Val	Glu	His	Ser	Phe	Ser
260		265		270											
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr
275		280		285											
Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp
290		295		300											
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
305		310		315		320									
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
325		330		335											
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser
340		345		350											
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Ser	Asn	Leu	Val
355		360		365											
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile
370		375		380											
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala
385		390		395		400									
Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val
405		410		415											
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg							
420		425													

<210> 11

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: heme binding motif

<220>

<221> UNSURE

<222> (2, 3)

<223> Xaa=unknown

<400> 11

Cys Xaa Xaa Cys His

<210> 12
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 12
catgccatgg cacacaacga caacac 26

<210> 13
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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gtcgacgatc ttcttccagc cgaacatcac 30

<210> 14
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<212> DNA
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<220>
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<210> 15
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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

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ttatttactc tcctgcggcg acaaatgtt 30